

Exhibit A

Clean Version of The Pending Claims in U.S. Patent Application Ser. No. 09/714,882

- 1.(Amended) An isolated nucleic acid molecule comprising the nucleotide sequence shown in SEQ ID NO:1.
- 2.(Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:2.
3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:4.
4. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:6.
- 5 An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:8.
6. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:10.
- 7.(New) An expression vector comprising a nucleic acid sequence of Claim 2.
- 8.(New) A cell comprising the expression vector of Claim 7.

Exhibit B

Marked-up Version of The Pending Claims in U.S. Patent Application Ser. No. 09/714,882

1. An isolated nucleic acid molecule comprising [at least 24 contiguous bases of] the nucleotide sequence [first disclosed in the NHP sequence described] shown in SEQ ID NO:1.
2. An isolated nucleic acid molecule comprising a nucleotide sequence that:
 - (a)]encodes the amino acid sequence shown in SEQ ID NO:2[; and
 - (b) hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof].
3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:4.
4. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:6.
5. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:8.
6. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:10.
- 7.(New) An expression vector comprising a nucleic acid sequence of Claim 2.
- 8.(New) A cell comprising the expression vector of Claim 7.

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NiceProt View of TrEMBL: Q9UGD3

SEP 16 2002

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[\[General\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#) [\[Features\]](#)
[\[Sequence\]](#) [\[Tools\]](#)

General information about the entry

Entry name **Q9UGD3**Primary accession number **Q9UGD3**Secondary accession numbers **None**Entered in TrEMBL in **Release 13, May 2000**Sequence was last modified in **Release 17, June 2001**Annotations were last modified in **Release 22, October 2002**

Name and origin of the protein

Protein name **DJ842G6.2 [Fragment]**Synonym **Novel protein imilar to SEL1L (Sel-1 (Suppressor of lin-12, C.elegans)-like)**Gene name **DJ842G6.2**From **Homo sapiens (Human) [TaxID: 9606]**Taxonomy **Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.**

References

[1] SEQUENCE FROM NUCLEIC ACID.

Barlow K.;

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

EMBL **AL109657; CAB65792.2; -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]**Genew **[HGNC:15897](#); [C20orf50](#).**Ensembl **Q9UGD3; Homo sapiens. [[Entry](#) / [Contig view](#)]**ProtoMap **[Q9UGD3](#).**PRESAGE **[Q9UGD3](#).**ModBase **[Q9UGD3](#).**SWISS-2DPAGE **[GET REGION ON 2D PAGE](#).**

Keywords

None

Features

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Key From To Length Description
NON_TER 1 1



Feature table viewer

Sequence information

Length: **505 AA** [This is the length of the partial sequence]
Molecular weight: **57003 Da** [This is the MW of the partial sequence]

CRC64: **536D4361FA826E35** [This is a checksum on the sequence]

10	20	30	40	50	60
ALGFLSSYGI	GMEYDQAKAL	IYYTFGSAGG	NMMSQMILGY	RYLSGINVLQ	NCEVALSYK
70	80	90	100	110	120
KVADYIADTF	EKSEGVPEK	VRLTERPENL	SSNSEILDWD	IYQYYKFLAE	RGDVQIQVSL
130	140	150	160	170	180
GQLHLIGRKG	LDQDYKALH	YFLKAAKAGS	ANAMAFIGKM	YLEGNAAVPQ	NNATAFKYFS
190	200	210	220	230	240
MAASKGNAIG	LHGLGLLYFH	GKGVPLNYAE	ALKYFQKAAE	KGWPDAQFQL	GFMYYSGSGI
250	260	270	280	290	300
WKDYKLAFKY	FYLASQSGQP	LAIYYLAKMY	ATGTGVVRSC	RTAVELYKGV	CELGHWAEEK
310	320	330	340	350	360
LTAYFAYKDG	DIDSSLVQYA	LLAEMGYEVA	QSNSAFILS	KKANILEKEK	MYPMALLLWN
370	380	390	400	410	420
RAAIQGNFA	RVKIGDYHY	GYGTKKDYQT	AATHYSIAAN	KYHNAQAMFN	LAYMYEHGLG
430	440	450	460	470	480
ITKDIHLARR	LYDMAAQTS	DAHIPVLFV	MKLETTHLLR	DILFFNFTR	WNWLKLDNTI
490	500				
GPHWDLFVIG	LIVPGLILL	RNHHG			

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Q9UGD3 in FASTA
format

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Direct BLAST submission at
EMBLnet-CH/SIB (Switzerland)



Direct BLAST submission at NCBI (Bethesda, USA)

Sequence analysis tools: ProtParam, ProtScale,

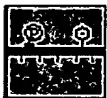


[ScanProsite](#), [MotifScan](#)

Tools



[Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#),
[Dotlet \(Java\)](#)



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Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

```
/tmp/fastaCAA_Xa40t: 689 aa
>FIRST_SEQUENCE
vs /tmp/fastaDAAaYa40t library
searching /tmp/fastaDAAaYa40t library
```

505 residues in 1 sequences

```
FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 38, opt: 26, gap-pen: -12/ -2, width: 16
Scan time: 0.033
```

The best scores are:

					opt
tr O9UGD3	DJ842G6.2	(Novel protein imilar to SEL1	(505)	3344	

```
>>tr|Q9UGD3 DJ842G6.2 (Novel protein imilar to SEL1L (Se (505 aa)
initn: 3342 initl: 3071 opt: 3344
Smith-Waterman score: 3344; 99.802% identity in 506 aa overlap (184-689:1-505)
```

```

      160          170          180          190          200          210
FIRST_ LFGNFGVQNITAAIQLYESLAKEGSCKAQNALGFLSSYGIGMEYDQAKALIYYTFGSAGG
      : ::::::::::::::::::::::::::::::::::::
tr|Q9U                                ALGFLSSYGIGMEYDQAKALIYYTFGSAGG
                                   10         20        30

```

FIRST_ NMMSQMILGYRYLSGINVLQNCCEVALSYKKVADYIADTFEKSEGVPEKVRLLTERPENL

 tr|Q9U NMMSQMILGYRYLSGINVLQNCCEVALSYKKVADYIADTFEKSEGVPEKVRLLTERPENL

280 290 300 310 320 330
 FIRST_ SSNSEILDWDIYQYYKFLAERGDVQIQVSLGQLHLIGRKGLDQDYKALHYFLKAAKAGS
 ::
 tr|Q9U SSNSEILDWDIYQYYKFLAERGDVQIQVSLGQLHLIGRKGLDQDYKALHYFLKAAKAGS
 100 110 120 130 140 150

FIRST_ ANAMAFIGKMYLEGNAAVPQNNATAFKYFSMAASKGNAIGLHGLGLLYFHHGKGVPPLNYAE
:::.....
tr|Q9U ANAMAFIGKMYLEGNAAVPQNNATAFKYFSMAASKGNAIGLHGLGLLYFHHGKGVPPLNYAE
 160 170 180 190 200 210

FIRST_ ALKYFQKAAEKGWPD AQFQLGFMYYSGSGIWKDYKLAFKYFYLASQSGQPLAIYYLAKMY
::: :::
tr|Q9U ALKYFQKAAEKGWPD AQFQLGFMYYSGSGIWKDYKLAFKYFYLASQSGQPLAIYYLAKMY
220 230 240 250 260 270

FIRST_ ATGTGVVRSCTAVELYKGVCELGHWAEEKFLTAYFAYKDGDIDSSLVQYALLAEMGYEVA
:
tr|Q9U ATGTGVVRSCTAVELYKGVCELGHWAEEKFLTAYFAYKDGDIDSSLVQYALLAEMGYEVA

460 470 480 490 500 510
280 290 300 310 320 330

520 530 540 550 560 570
FIRST_QSNSAFILESKKANILEKEKMPMALLLWNRAAIQGNAFARVKIGDYHYYGYGTTKKDYQT

```

.....
tr|Q9U QSNSAFILESKKANILEKEKMPMALLLWNRAAIQGNAFARVKIGDYHYGYGTTKKDYQT
      340      350      360      370      380      390

      580      590      600      610      620      630
FIRST_ AATHYSIAANKYHNAQAMFNLAYMYEHGLGITKDIHLARRLYDMAAQTSPDAHIPVLFVAV
      .....
tr|Q9U AATHYSIAANKYHNAQAMFNLAYMYEHGLGITKDIHLARRLYDMAAQTSPDAHIPVLFVAV
      400      410      420      430      440      450

      640      650      660      670      680
FIRST_ MKLETTHLLRDILFFNQFTTRWNWLKLDNTIGPHWDLFVIGLIVPGLILLLRNHHG
      .....
tr|Q9U MKLETTHLLRDILFFN-FTTRWNWLKLDNTIGPHWDLFVIGLIVPGLILLLRNHHG
      460      470      480      490      500

```

689 residues in 1 query sequences
 505 residues in 1 library sequences
 Scomplib [version 3.3t05 March 30, 2000]
 start: Fri Sep 6 11:53:40 2002 done: Fri Sep 6 11:53:40 2002
 Scan time: 0.033 Display time: 0.434

Function used was FASTA